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      | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
356 EVSEEDHDPYLKAVYLEGLRKHPPAHMLLPHKAAEDMDVGYLIPKCTIVNFMVAENG 415

QY 91 SQ-----DCAGTD 98

Db 416 RDEKEWKPMEFMPERFLPGGDGEYD 442

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RESULT 14
ID 051827 PRELIMINARY; PRT; 2458 AA.
AC 051827;
DT 01-JUN-1998 (Tremblrel. 06, Created)
DT 01-JUN-1998 (Tremblrel. 06, Last sequence update)
DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
DE Polyketide synthase type I.
GN PLTB.
OS Pseudomonas fluorescens.
OC Bacteria; Proteobacteria; gamma subdivision; pseudomonadaceae;
OC Pseudomonas.
OX NCBI_TaxID=294;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=PF-5;
RX MEDLINE=98034250; Pubmed=9434161;
RA Nowak-Thompson B., Gould S.J., Loper J.E.;
RA "Identification and sequence analysis of the genes encoding a
RT polyketide synthase required for pyoluteorin biosynthesis in
RT Pseudomonas fluorescens Pf-5.";
RL Gene 204:117-24(1997).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=PF-5;
RX MEDLINE=99194726; Pubmed=10094695;
RA Nowak-Thompson B., Chaney N., Wing J.S., Gould S.J., Loper J.E.;
RA "Characterization of the pyoluteorin biosynthetic gene cluster
RT in Pseudomonas fluorescens Pf-5.";
RL J. Bacteriol. 181:2166-2174(1999).
DR EMBL; AF081920; AC38075.1; -
DR InterPro; IPR001127; AC.transferase.
DR InterPro; IPR000794; ketoacyl-synt.
DR InterPro; IPR003880; Ppantne.attach.
DR InterPro; IPR002155; Thiolase..
DR Pfam; PF00698; Acyl_transf. 1.
DR Pfam; PF00109; ketoacyl-synt; 2.
DR Pfam; PF02801; ketoacyl-synt_C; 2.
DR Pfam; PF00550; pp-binding; 2.
DR PROSITE; PS00075; ACP_DOMAIN; 2.
DR PROSITE; PS00606; B_KETOACYL-SYNTHASE; 2.
DR PROSITE; PS00012; PHOSPHOPANTHETHEINE; UNKNOWN_1.
DR PROSITE; PS00098; THIOLASE_1; UNKNOWN_1.
DR Phosphopantetheine; Transferase.
SQ SEQUENCE 2458 AA; 262676 MW; AE756080AE1ASFE1 CRC64;

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Query Match	12.8%	Score 69.5;	DB 2;	Length 2458;
Best Local Similarity	32.1%	Pred. No. 2.4e+02;		
Matches 17;	Conservative 14;	Mismatches 19;	Indels 3;	Gaps 2;

Qy 44 ELYEGTIGKYNVNEDAKAAMTELKSCIDGLQPMHKAELVKLLVQLVGLSQDGAG 96
: | : : : | | | : | | | : : : : : | | | |

Db 2239 QLLHLTQSEQELEDA-AARTAMQG--SGLOPLORSQIVQAIARVLGGGQCG 2288

RESULT 15	
Q9CFY4	
ID	PRELIMINARY:
AC	PRT; 540 AA.
Q9CFY4;	
DT 01-JUN-2001	(TrEMBLrel. 17, Created)
DT 01-JUN-2001	(TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2002	(TrEMBLrel. 20, Last annotation update)
DE	Fibronectin-binding protein.
DE	YNGB OR LL1327.
OS	Lactococcus lactis (subsp. lactis) (Streptococcus lactis).

	Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
OC	Streptococcaceae; Lactococcus.
OX	NCBI_TaxID=1360;
XX	[1]
RN	SEQUENCE FROM N.A.
RP	STRAIN=IL1403;
RQ	MEDLINE=21235186; PubMed=11373471;
RX	RA Bolotin A., Wincker P., Mauger S., Jaillon O., Malarme K.,
RY	Weissenbach J., Ehrlich S.D., Sorokin A.;
SA	Lactis ssp. lactis IL1403.;
SB	Genome Res. 11:731-753(2001).
SC	EMBL; AE0063165; AAAK05425.1; -.
SF	Complete proteome.
SK	SEQUENCE 540 AA; 61285 MW; 4DAC3CCBCF72867 CRC64;
SL	Query Match 12.7%; Score 69; DB 16; Length 540;
SM	Best Local Similarity 30.6%; Pred.No. 41;
SN	Matches 22; Conservative 9; Mismatches 37; Indels 4; Gaps
SO	25 DNEBF--DFTQLVGTPEELVECTGLGYNVEDAKAAMTELKSICDIGLQP-MHKAEE 80 : : :
SP	294 DNAEIPRKGELENTLNQVNPDKTSTVLNVYTNTEPIALNPALSVPONAQRVHYRHO 353 : : :

Query Match 12.7%; Score 69; DB 16; Length 540;
Best Local Similarity 30.6%; Pred. No. 41;
Matches 22: Conservative 9; Mismatches 37; Indels

Qy	25	DNDEFM---DFLOTLLVGTPEELYEGTLCKYVNVEDAKAAMTELKSCIDGLQP-MHKAE	80
Db	294	DNAEIFRQKGELENTFLNVPDKTSTVLENYTTPETIEALNPALSPVONARQYFHRQY	353
Qy	81	LVKLLVQVLGSQ	92
Db	354	KLRQAVKFLGEO	365

Search completed: May 14, 2003, 10:52:40
Job time : 37 secs

RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojohori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda K., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gliss C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Stauble F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Harsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein S.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzairelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.
RT "Functional annotation of a full-length mouse cDNA collection."
RL Nature 409:685-690(2001).
RN [2]
RP SEQUENCE FROM N.A.
RL Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK011928; BAB27921.1; -
DR EMBL; BC019683; AAL19683.1; -
DR HSSP; 007347; 2EPH.
DR MGD; MGI:1345087; Srp54.
DR InterPro; IPR003593; AAA_ATPase.
DR InterPro; IPR000897; SRP54.
DR InterPro; IPR004125; SRP54_SPB.
DR Pfam; PF00448; SRP54; 1.
DR Pfam; PF02881; SRP54_N; 1.
DR Pfam; PF02978; SRP_SPB; 1.
DR ProDom; PD000819; SRP54; 1.
DR SMART; SM00382; AAA; 1.
DR PROSITE; PS00300; SRP54; 1.
SQ SEQUENCE 504 AA; 55720 MW; 79AD58BE6D1E89CA CRC64;
Query Match 14.1%; Score 76.5; DB 11; Length 504;
Best Local Similarity 32.4%; Pred. No. 5.5;
Matches 36; Conservative 16; Mismatches 40; Indels 19; Gaps 6;
Qy 2 KGSRALLVLTLCICRMATGDNDEF----FMDFLQTLV-VGTPELYECTLGKYNVN 56
Db 255 KGGGALSAAVATKSPFIIGTGHIDDPFKTQPFISKLLMGDIEGLID-----KVN 308
Qy 57 E----DAKAAMTELKSCIDGLQPMHK--AELVKL--LVQVLGSDGAGTDY 99
Db 309 ELKLDNEALIEKLUKGQFTLRDMEQFNIMKMGPFSSQILGMIPGFGTDF 359
RESULT 6
ID Q8XM24 PRELIMINARY; PRT; 2104 AA.
AC Q8XM24
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Probable alpha-N-acetylglucosaminidase.
GN CPE0866.
OS Clostridium perfringens.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia;
OC Clostridiales; Clostridiaceae; Clostridium.
OX NCBI_TaxID=1502;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=13 / TYPE A;
RX PubMed=11792842;
RA Shiba T., Ogasawara N., Hattori M., Kuhara S., Hayashi H.,
RA Shiba T., Ohtani K., Hirakawa H., Ohshima K., Yamashita A.,
RT "Complete genome sequence of Clostridium perfringens, an anaerobic
flesh-eater."
RL Proc. Natl. Acad. Sci. U.S.A. 99:996-1001(2002).
DR EMBL; AP003188; BAB80572.1; -

DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR000421; FAS8_C.
DR InterPro; IPR003961; FN_III.
DR Pfam; PF00754; F5_F8_type_C; 1.
DR Pfam; PF00041; fn3; 1.
DR SMART; SM00060; FN3; 1.
DR PROSITE; PS00018; EF_HAND; UNKNOWN_1.
KW Complete proteome.
SQ SEQUENCE 2104 AA; 236010 MW; 5FE345659599EED7 CRC64;
Query Match 14.0%; Score 76; DB 16; Length 2104;
Best Local Similarity 29.0%; Pred. No. 38;
Matches 27; Conservative 10; Mismatches 34; Indels 22; Gaps 3;
Qy 24 EDNDEF--FMDFLQTLVGTPELYECTLGKYNVNEDAKAAMTELKSCIDGLQPMHKA 80
Db 721 KDSDAFLVDFADILKQLLANSQAQYEVCMNAYNNGNGEKFKFVSGKF-----LE 770
Qy 81 LVKLLVQVLGSDQ-----DGAGTDYKDDDD 104
Db 771 LIKQLQVRLSTRPEFLIGNWIEDARTMLKDSDD 803
RESULT 7
ID Q9VAB8 PRELIMINARY; PRT; 457 AA.
AC Q9VAB8
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE CG7928 protein (LD15405P).
GN CG7928.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Anantides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Aghayani A., An H.-J., Andrews-Pfannkuch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottlie P.,
RA Burtis K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Fosler C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Iqbalwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Li X., Li Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacht J.M.,
RA Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,

DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Potential ligand-binding protein.
GN RYDS.
OS Rattus rattus (Black rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10117;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FISCHER; TISSUE=OLFACTORY EPITHELIUM;
RX MEDLINE=92007724; PubMed=1915284;
RA Dear T.N., Boehm T., Keverne E.B., Rabbitts T.H.;
RT "Novel genes for potential ligand-binding proteins in subregions of
RT the olfactory mucosa."
RL EMBO J. 10:2813-2819(1991).
DR EMBL; X60661; CAA43068.1;
DR InterPro; IPR000329; Uterogloblin.
DR SMART; SM00096; UTG; 1.
SQ SEQUENCE 94 AA; 10401 MW; 25A4BBB4977E247 CRC64;
Query Match 64.5%; Score 349.5; DB 11; Length 94;
Best Local Similarity 75.3%; Pred. No. 3e-31;
Matches 70; Conservative 11; Mismatches 11; Indels 1; Gaps 1;
QY 1 MKGSRALLVALFICRMATGEDNDFMDFLQTLVGTPEELVGTGKYNVEDAK 60
Db 1 MKGSSA-LLVALVLCIGLTRAEDNEFFMDFLQTLVGTPEELVGTGKYNVEDAK 59
QY 61 AMTELKSCIDGLOPMHKAELVLLVQLGSD 93
Db 60 AALTELKSCIDGLOPMHKAELVLLVQLGSD 92
RESULT 3
Q8VD96 PRELIMINARY; PRT; 96 AA.
ID Q8VD96
AC Q8VD96;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DE C10 protein precursor.
DE CC10.
GN Mesocricetus auratus (Golden hamster).
OS Mesocricetus auratus (Golden hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Mesocricetus.
OX NCBI_TaxID=10036;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LUNG;
RA Gutierrez-Sagal R., Nieto A.;
RT "Cloning and sequencing of a cDNA encoding hamster uteroglobin/clara
RT cell 10 kDa protein."
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; L37041; AAL31349.1;
DR InterPro; IPR003628; Uteroglobn_sub.
DR InterPro; IPR000329; Uterogloblin.
DR Pfam; PF01099; Uterogloblin; 1.
DR ProDom; PD012475; Uteroglobn_sub; 1.
DR SMART; SM00096; UTG; 1.
DR PROSITE; PS00404; UTEROGLOBIN_2; UNKNOWN_1.
KW Signal.
FT SIGNAL
SQ SEQUENCE 96 AA; 10509 MW; 5EB9CBDD46143389 CRC64;
Query Match 16.7%; Score 90.5; DB 11; Length 96;
Best Local Similarity 27.8%; Pred. No. 0.019;
Matches 25; Conservative 17; Mismatches 43; Indels 5; Gaps 2;
QY 8 LLVALTFCICRMATGEDNDFMDFLQTLVGTPEELVGTGKYNVEDAKAMTELK 67
Db 5 ITMAVVLVSCSSASSSTCTGFFQVLEFLFMGS-ESSYEALAFYNPGSLQDSGTOLK 63

QY 68 SCIDGLOPMHKAELVLLVQLGSD 93
Db 64 KIVDTLPKTRNMIMKLSIILTSPLCNQD 93
RESULT 4
O62571 PRELIMINARY; PRT; 478 AA.
ID O62571
AC O62571;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DE Stress-responsive protein kinase (PRKSD).
DE Substrates domuncula (Sponge).
OC Eukaryota; Metazoa; Porifera; Demospongiae; Tetractinomorphia;
OC Hadromerida; Suberitidae; Suberites.
OX NCBI_TaxID=55567;
RN [1]
RP SEQUENCE FROM N.A.
RA Mueller W.E.G.;
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=96394688; PubMed=8798342;
RA Kruse M., Gamulin V., Cetkovic H., Pancer Z., Mueller I.M.,
RA Mueller W.E.G.;
RT "Molecular evolution of the Metazoan protein kinase C multigene
RT family."
RL J. Mol. Evol. 43:374-383(1996).
DR EMBL; Y13101; CAA73555.1;
DR HSP; P24941; IHCL.
DR InterPro; IPR000719; Euk_pkinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR Pfam; PF00069; pkinase; 1.
DR ProDom; PD000001; Euk_pkinase; 1.
DR SMART; SM00220; S_TKC; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
KW ATP-binding; Kinase; Transferase.
SQ SEQUENCE 478 AA; 54098 MW; 6B38FF5FD88D6332 CRC64;
Query Match 16.1%; Score 87.5; DB 5; Length 478;
Best Local Similarity 31.0%; Pred. No. 0.31;
Matches 27; Conservative 18; Mismatches 25; Indels 17; Gaps 4;
QY 22 TGEDNDEF---FMDFLQTLVGTPEELVGTGKYNVEDAKAMTELKSCIDGLOPMH 77
Db 238 TLKDTDKFSNEFSDFTSRCLVKNPEERMSATALLQHKFIKSAK-PVAVLK----- 286
QY 78 KAEVLVQLGSDGAGTDYKDDDD 104
Db 287 --ELIQDAMRILEEEGGSGDEEDND 311
RESULT 5
Q9D008 PRELIMINARY; PRT; 504 AA.
ID Q9D008
AC Q9D008;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DE Signal recognition particle 54 kDa.
DE SRP54.
GN Mus musculus (Mouse).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=EMBRYO;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shingagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

Result	Query	Score	Match	Length	DB	ID	Description
1	Q8TD33	477	88.0	95	4	Q8TD33	Q8TD33 homo sapien
2	Q05702	349.5	64.5	94	11	Q05702	Q05702 rattus ratt
3	Q8VD96	90.5	16.7	96	11	Q8VD96	Q8VD96 mesocricetu
4	Q62571	87.5	16.1	478	5	Q62571	Q62571 suberites d
5	Q9D008	76.5	14.1	504	11	Q9D008	Q9D008 mus musculu
6	Q8XM24	76	14.0	2104	16	Q8XM24	Q8XM24 clostridium
7	Q9VAB8	74	13.7	457	5	Q9VAB8	Q9VAB8 drosophila
8	Q9GK67	73	13.5	90	6	Q9GK67	Q9GK67 oryctolagus
9	Q9UR83	73	13.5	609	3	Q9UR83	Q9UR83 schizosacch
10	Q993Z9	72.5	13.4	500	11	Q993Z9	Q993Z9 mus musculu
11	Q8QXL2	70.5	13.0	3071	12	Q8QXL2	Q8QXL2 sorghum mos
12	Q8QX11	70.5	13.0	3071	12	Q8QX11	Q8QX11 sorghum mos
13	Q9FW93	69.5	12.8	643	10	Q9FW93	Q9FW93 oryza sativ
14	Q51827	69.5	12.8	2458	2	Q51827	Q51827 pseudomonas
15	Q9CFY4	69	12.7	540	16	Q9CFY4	Q9CFY4 lactococcus
16	P87112	68.5	12.6	2100	3	P87112	P87112 schizosacch

DT	01-NOV-1996 (TrEMBLrel. 01, Created)
DT	01-NOV-1996 (TrEMBLrel. 01, Last sequence update)

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Best Local Similarity 32.1%; Pred. No. 1.2e+02;
Matches .17; Conservative 14; Mismatches 19; Indels 3; Gaps 2;

QY 44 ELYEGTLGKYNNVEDAKAAMTELKSCIDGLQPMHKAELVLLVQVLGSDCAG 96
      :| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 2239 QLLHLTQSEGLEQDA-AARTAMOG--SGLOPLQRSQIVQAIARVLGGQCG 2288

RESULT 15
G86790
fibronectin-binding protein [imported] - Lactococcus lactis subsp. lactis (strain IL1403)
C:Species: Lactococcus lactis subsp. lactis
C>Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001
C:Accession: G86790
R:Boilotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; Ehrlich
Genome Res. 11, 731-753, 2001
A:Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis s
A:Reference number: A86625; MUID:21235186; PMID:11337471
A:Accession: G86790
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-540 <STO>
A:Cross-references: GB:AE005176; PID:g12724308; PIDN:AAK05425.1; GSPDB:GNO0146
A:Experimental source: strain IL1403
C:Genetics:
A:Gene: yngB

Query Match 12.7%; Score 69; DB 2; Length 540;
Best Local Similarity 30.6%; Pred. No. 25;
Matches 22; Conservative 9; Mismatches 37; Indels 4; Gaps 2;

QY 25 DNDDEFFM---DFLOTLLVGTPEELYEGTLGKYNNVEDAKAAMTELKSCIDGLQPMHKA 80
      ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 294 DNAEIFRQKGLLTLNQLQVNDKTSVTLENYTNEPIALNPALSPVQNAQRYPHRYQ 353

QY 81 LVKLLVQVLGSO 92
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Db 354 KLQAVKFLGEQ 365

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Search completed: May 14, 2003, 10:53:02
Job time : 19 secs

R:Bernstein, H.

Submitted to the EMBL Data Library, November 1989

A:Reference number: S14553

A:Accession: S14553

A:Molecule type: mRNA

A:Residues: 1-42, 'DV', 45-504 <BER2>

A:Cross-references: EMBL:X16319; NID:g54193; PIDN:CAA34386.1; PID:g54194

C:Superfamily: signal recognition particle 54K protein

F:2-504/Product: signal recognition particle 54K protein #status predicted <MAT>

Query Match 14.1%; Score 76.5; DB 2; Length 504;

Best Local Similarity 32.4%; Pred. No. 3.7;

Matches 36; Conservative 16; Mismatches 40; Indels 19; Gaps 6;

QY 2 KGSRALLLVLTFCICRMATGEDNDEF----FMDFLQTL--VGTPEELYECTLGKYNVN 56

DB 255 KGGGALSAVAATKSPFIIFGTGEHIDDFEPTQTQPFISKLLMGDIEGLID-----KVN 308

QY 57 E----DAKAAMTELKSCIDGLQPMHK--AELVKL--LVQVLGSDGAGTDY 99

DB 309 ELKLDNEALIEKLKHGQFTLRDMYEQFQNTMKMGPFQILGMIPFGTDF 359

RESULT 11

S54143

SRP 54 protein - human (fragment)

C:Species: Homo sapiens (man)

A:Reference number: S54143

A:Accession: S54143

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-504 <PAT>

A:Cross-references: EMBL:X86373; NID:g784998; PIDN:CAA60132.1; PID:g784999

C:Superfamily: signal recognition particle 54K protein

Query Match 14.1%; Score 76.5; DB 2; Length 504;

Best Local Similarity 32.4%; Pred. No. 3.7;

Matches 36; Conservative 16; Mismatches 40; Indels 19; Gaps 6;

QY 2 KGSRALLLVLTFCICRMATGEDNDEF----FMDFLQTL--VGTPEELYECTLGKYNVN 56

DB 255 KGGGALSAVAATKSPFIIFGTGEHIDDFEPTQTQPFISKLLMGDIEGLID-----KVN 308

QY 57 E----DAKAAMTELKSCIDGLQPMHK--AELVKL--LVQVLGSDGAGTDY 99

DB 309 ELKLDNEALIEKLKHGQFTLRDMYEQFQNTMKMGPFQILGMIPFGTDF 359

RESULT 12

T38656

Probable RNA-binding protein - fission yeast (Schizosaccharomyces pombe)

C:Species: Schizosaccharomyces pombe

C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999

C:Accession: T38656

R:Murphy, L.; Harris, D.; Wood, V.; Rajandream, M.A.; Barrell, B.G.

Submitted to the EMBL Data Library, August 1997

A:Reference number: Z21804

A:Accession: T38656

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-609 <MUR>

A:Cross-references: EMBL:AL109739; NID:el534774; PIDN:CAB52270.1; GSPDB:GN00066; SPDB:SH

A:Experimental source: strain 972h-; cosmid c343

C:Genetics:

A:Gene: SPDB:SPAC343.07

A:Map position: 1

A:Introns: 44/1; 96/2; 325/3

Query Match 13.5%; Score 73; DB 2; Length 609;

Best Local Similarity 23.5%; Pred. No. 11;

Matches 23; Conservative 20; Mismatches 27; Indels 28; Gaps 5;

QY 18 CRMATG---EDNDEFFMDFLQTLVVG-----TPEELYE-----GTLGKYNVNE 57

DB 248 COMPGMLLEQNQPLDYNDNPSIFVIGILNPLKVPVELYNFESNHGHLGVAINQSINE 307

QY 58 D----AKAAMTELKSCIDGLQPMH-----KAELVKLLVQ 87

DB 308 DMTHAEVAVSTYESCIEIIEKFAHAYEGSILQFIK 345

RESULT 13

S41122

mannose-6-phosphate isomerase (EC 5.3.1.8) - human

N:Alternate names: phosphomannose isomerase

C:Species: Homo sapiens (man)

C:Date: 07-Sep-1994 #sequence_revision 10-Nov-1995 #text_change 08-Oct-1999

C:Accession: S41122; S38666

R:Proudfoot, A.E.I.; Turcatti, G.; Wells, T.N.C.; Payton, M.A.; Smith, D.J.

Eur. J. Biochem. 219, 415-423, 1994

A:Title: Purification, cDNA cloning and heterologous expression of human phosphomanno

A:Reference number: S41122; MUID:94139717; PMID:8307007

A:Accession: S41122

A:Molecule type: mRNA

A:Residues: 1-423 <PRO>

A:Cross-references: EMBL:X76057; NID:g416016; PIDN:CAA53657.1; PID:g416017

C:Genetics:

A:Gene: GDB:MPI

A:Cross-references: GDB:I19397; OMIM:154550

A:Map position: 15q22-15qter

C:Superfamily: yeast mannose-6-phosphate isomerase

C:Keywords: intramolecular oxidoreductase; Isomerase

Query Match 13.0%; Score 70.5; DB 2; Length 423;

Best Local Similarity 25.7%; Pred. No. 13;

Matches 27; Conservative 19; Mismatches 38; Indels 21; Gaps 5;

QY 8 LLVALTLF-CICRMATGEDNDEFMDFLQTLVGTPEELYECTLG-----KYNVNEDA 59

DB 138 MAIALTFPGGLGCGRPVEE-----IVTFLKKVPE--FOFLIGDEANTHLKOTMSHDS 187

QY 60 KAAMTELKSCIDGLQPMHK-----AELVKLLVQVLGSDGAGTDYKD 101

DB 188 QAVASSLQSCFSLMKSEKVVVEQLNLLVKRISQQAAGNMED 232

RESULT 14

T17420

Probable polyketide synthase type I - Pseudomonas fluorescens

C:Species: Pseudomonas fluorescens

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 17-Nov-2000

C:Accession: T17420

R:Nowak-Thompson, B.; Chaney, N.; Wing, J.S.; Gould, S.J.; Loper, J.E.

J. Bacteriol. 181, 2166-2174, 1999

A:Title: Characterization of the pyoluteorin biosynthetic gene cluster of pseudomonas

A:Reference number: Z18776; MUID:99194726; PMID:10094695

A:Accession: T17420

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-2458 <NOW>

A:Cross-references: EMBL:AF081920; NID:g4582974; PID:g2781416; PIDN:AAC38075.1

C:Genetics:

A:Gene: pltB

C:Superfamily: 3-oxoacyl-[acyl-carrier-protein] synthase I homology; acyl carrier pro

C:Keywords: carrier protein

F:31-429/Domain: 3-oxoacyl-[acyl-carrier-protein] synthase I homology <OAS1>

F:535-815/Domain: lacyl-carrier-protein] S-malonyltransferase homology <OAS1>

F:939-1009/Domain: acyl carrier protein homology <ACP1>

F:1053-1446/Domain: 3-oxoacyl-[acyl-carrier-protein] synthase I homology <OAS2>

F:2337-2408/Domain: acyl carrier protein homology <ACP2>

Query Match 12.8%; Score 69.5; DB 2; Length 2458;

A:Cross-references: GB:L04503; NID:g202313; PIDN:AAA03625.1; PID:g433093
C:Genetics: 19/1; 81/3
A:Introns:
C:Complex: homodimer linked by two disulfide bonds
C:Superfamily: uteroglobin
C:Keywords: lung; steroid binding; uterus
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-96/Product: uteroglobin #status predicted <MAT>
F:24/Disulfide bonds: interchain (to 90) #status predicted
F:90/Disulfide bonds: interchain (to 24) #status predicted

Query Match 15.0%; Score 81.5; DB 1; Length 94;
Best Local Similarity 26.2%; Pred. No. 0.17;
Matches 22; Conservative 19; Mismatches 42; Indels 1; Gaps 1;

QY 8 LLVALTLCICRMATGEDNDEFFMDFLQTLVGTPELYEGTLGKYNVELAKAAMTELK 67
DB 5 ITTVVMSICCSASSDPCGFLQVLEALLMES-ESGVASLKPFNPGSDLNAGTOLK 63

QY 68 SCIDGLQPMHKAELVLLVQVLGS 91
DB 64 RLVDTLPOETRINIMKLEIKILTS 87

RESULT 7
JGRBL
uteroglobin precursor - brown hare
N:Alternate names: blastokinin
C:Species: Lepus capensis (brown hare)
C:Date: 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 22-Jun-1999
C:Accession: A23825
R:Lopez de Haro, M.S.; Nieto, A.
Biochem. J. 235, 893-898, 1986
A:Title: Nucleotide and derived amino acid sequences of a cDNA coding for pre-uteroglobin
A:Reference number: A23825; MUID:86323069; PMID:3019311
A:Accession: A23825
A:Molecule type: mRNA
A:Residues: 1-91 <LOP>
A:Cross-references: GB:M25609; NID:g164246; PIDN:AAA30960.1; PID:g164247
A:Experimental source: lung
C:Comment: Uteroglobin, synthesized in the uterus and lung, is secreted by the uterus ut
C:Complex: homodimer linked by two disulfide bonds
C:Superfamily: uteroglobin
C:Keywords: lung; steroid binding; uterus
F:1-21/Domain: signal sequence #status predicted <SIG>
F:22-91/Product: uteroglobin #status predicted <MAT>
F:24/Disulfide bonds: interchain (to 90) #status predicted
F:90/Disulfide bonds: interchain (to 24) #status predicted

Query Match 14.8%; Score 80; DB 1; Length 91;
Best Local Similarity 26.8%; Pred. No. 0.23;
Matches 26; Conservative 18; Mismatches 37; Indels 16; Gaps 3;

QY 1 MKGSRALLLVALTLC-----ICRMATGEDNDEFFMDFLQTLVGTPELYEGTLGKYN 54
DB 1 MKLTITLALVTLALCSPASAGIC-----PGFAHVIENTLLGTPSS-YGTSLEKFEQ 50

QY 55 VNEDAKAAMTELKSCIDGLQPMHKAELVLLVQVLGS 91
DB 51 PDDAMKDAGMQMKVLDLTPQTTRENIKIILTEIKIVKS 87

RESULT 8
JC2026
cell specific 10K protein - mouse
C:Species: Mus musculus (house mouse)
C:Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 17-Mar-1999
C:Accession: JC2026
R:Ray, M.K.; Magdaleno, S.; O'Malley, B.W.; DeMayo, F.J.
Biochem. Biophys. Res. Commun. 197, 163-171, 1993
A:Title: Cloning and characterization of the mouse clara cell-specific 10 kDa protein ge
A:Reference number: JC2026; MUID:94071937; PMID:7916613
A:Accession: JC2026

A:Molecule type: DNA
A:Residues: 1-113 <RAY>
C:Comment: This protein is the major secretory product of the Clara cell and binds to
C:Superfamily: uteroglobin
F:73/Region: ochre stop codon

Query Match 14.5%; Score 78.5; DB 2; Length 113;
Best Local Similarity 30.7%; Pred. No. 0.43;
Matches 27; Conservative 15; Mismatches 43; Indels 3; Gaps 2;

QY 6 ALLVALTLCICRMATGEDND--EFFMDFLQTLVGTPELYEGTLGKYNVEDAKAAM 63
DB 18 SLEKLLSFCFFLPATPASSDPCGFLQVLEALLMES-ESGVASLKPFNPGSDLNAG 76

QY 64 TELKSCIDGLQPMHKAELVLLVQVLGS 91
DB 77 TOLKRLVDTLPOETRINIMKLEIKILTS 104

RESULT 9
S05197
signal recognition particle 54K protein - dog
C:Species: Canis lupus familiaris (dog)
C:Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 02-Feb-2001
C:Accession: S05197; SI0619
R:Roemisch, K.; Webb, J.; Herz, J.; Prehn, S.; Frank, R.; Vingron, M.; Dobberstein, B
Nature 340, 478-482, 1989
A:Title: Homology of 54K protein of signal-recognition particle, docking protein and
A:Reference number: S05197; MUID:89330596; PMID:2502717
A:Accession: S05197
A:Molecule type: mRNA
A:Residues: 1-504 <ROE>
A:Cross-references: EMBL:X16318; NID:g928; PIDN:CAA34385.1; PID:g930
A:Note: part of this sequence, including the amino end of the mature protein, was con
R:Bernstein, H.D.; Poritz, M.A.; Strub, K.; Hoben, P.J.; Brenner, S.; Walter, P.
Nature 340, 482-486, 1989
A:Title: Model for signal sequence recognition from amino-acid sequence of 54K subuni
A:Reference number: S05198; MUID:89330597; PMID:2502718
A:Accession: SI0619
A:Molecule type: protein
A:Residues: 2-35; 58-70; 120-126; 141-153; 374-388; 416-426; 470-485 <BER>
C:Superfamily: signal recognition particle 54K protein
C:Keywords: GTP binding; nucleotide binding; P-loop
F:1-504/Product: signal recognition particle 54K protein #status experimental <MAT>
F:108-115/Region: nucleotide-binding motif A (P-loop)

Query Match 14.1%; Score 76.5; DB 2; Length 504;
Best Local Similarity 32.4%; Pred. No. 3.7;
Matches 36; Conservative 16; Mismatches 40; Indels 19; Gaps 6;

QY 2 KGSRALLLVALTLCICRMATGEDNDEFFMDFLQTLVGTPELYEGTLGKYNVN 56
DB 255 KGGGALSAAVATKSPIIFIGTGEHIDDFEPTKTPPFISKLLGMGMDIEGLID-----KVN 308

QY 57 E-----DAKAAMTELKSCIDGLQPMHK--AELVKL--LVQVLGSQDGAGTDY 99
DB 309 ELKLDNDNEALIEKLKHGQFTLRDMYEQFNIMKMGPPSQILGMIPGFGTDF 359

RESULT 10
S05198
signal recognition particle 54K protein - mouse
C:Species: Mus musculus (house mouse)
C:Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 23-Jul-1999
C:Accession: S05198; SI4553
R:Bernstein, H.D.; Poritz, M.A.; Strub, K.; Hoben, P.J.; Brenner, S.; Walter, P.
Nature 340, 482-486, 1989
A:Title: Model for signal sequence recognition from amino-acid sequence of 54K subuni
A:Reference number: S05198; MUID:89330597; PMID:2502718
A:Accession: S05198
A:Molecule type: mRNA
A:Residues: 1-504 <BER1>
A:Cross-references: EMBL:X16319

A:Reference number: A24217; MUID:86056319; PMID:2415398
A:Accession: A24217
A:Molecule type: mRNA
A:Residues: 22-91 <LOP>
A:CROSS-references: GB:M27564; NID:g165792; PIDN:AAA31496.1; PID:g165793
A:Experimental source: lung
R:Atger, M.; Mercier, J.C.; Haze, G.; Fridlansky, F.; Milgrom, E.
Biochem. J. 177, 985-988, 1979
A:Title: N-terminal sequences of uteroglobin and its precursor.
A:Reference number: A90303; MUID:79187160; PMID:571719
A:Accession: A90303
A:Molecule type: protein
A:Residues: 1-5, '7-10, 'X', '15, 'G', '17-54, 'X', '56, 'B', '58-66, 'B', '68-70, 'XX', '73 <ATC>
R:Ponstingl, H.; Nieto, A.; Beato, M.
Biochemistry 17, 3908-3912, 1978
A:Title: Amino acid sequence of progesterone-induced rabbit uteroglobin.
A:Reference number: A90417; MUID:79042086; PMID:568483
A:Accession: A90417
A:Molecule type: protein
A:Residues: 22-81, 'Q', '83-91 <PON>
R:Popp, R.A.; Foresman, K.R.; Wise, L.D.; Daniel Jr., J.C.
Proc. Natl. Acad. Sci. U.S.A. 75, 5516-5519, 1978
A:Title: Amino acid sequence of a progesterone-binding protein!
A:Reference number: A93824; MUID:79074850; PMID:281700
A:Accession: A93824
A:Molecule type: protein
A:Residues: 22-49, 'D', '51, 'EN', '54-59, '61-66, 'NEPSL', '72-91 <POP>
R:Popp, R.A.; Foresman, K.R.; Wise, L.D.; Daniel Jr., J.C.
submitted to the Atlas, October 1982
A:Reference number: A94608
A:Accession: A94608
A:Molecule type: protein
A:Residues: 50-62; 67-71 <PO2>
R:Morize, I.; Surcouf, E.; Vaney, M.C.; Buehner, M.; Morrison, J.P.
submitted to the Brookhaven Protein Data Bank, April 1989
A:Reference number: A50025; PDB:1UTG
R:Morize, I.; Surcouf, E.; Vaney, M.C.; Epelboin, Y.; Buehner, M.; Fridlansky, F.; Milgrom, E.
J. Mol. Biol. 194, 725-739, 1987
A:Title: Refinement of the C222-1 crystal form of oxidized uteroglobin at 1.34 angstroms
A:Reference number: A44652; MUID:88011213; PMID:3656405
A:Contents: annotation: X-ray crystallography, 1.34 angstroms
R:Bally, R.; Delettre, J.
submitted to the Brookhaven Protein Data Bank, May 1989
A:Reference number: A50553; PDB:2UTG
A:Contents: annotation: X-ray crystallography, 1.64 angstroms, residues 22-91
R:Bally, R.; Delettre, J.
J. Mol. Biol. 206, 153-170, 1989
A:Title: Structure and refinement of the oxidized P2-1 form of uteroglobin at 1.64 angstroms
A:Reference number: A44653; MUID:89199637; PMID:2704039
A:Contents: annotation: X-ray crystallography, 1.64 angstroms; disulfide bonds
R:Kenne, C.; Suske, G.; Arnemann, J.; Wenz, M.; Cato, A.C.B.; Beato, M.
Proc. Natl. Acad. Sci. U.S.A. 79, 4853-4857, 1982
A:Title: Isolation and structure of the gene for the progesterone-inducible protein uteroglobin
A:Reference number: I46904; MUID:83014950; PMID:6956897
A:Accession: I46904
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-91 <MEN>
A:CROSS-references: GB:J00689; NID:g165786; PIDN:AAA31495.1; PID:g165788
R:Chandra, T.; Woo, S.L.C.; Bullock, D.W.
Biochem. Biophys. Res. Commun. 95, 197-204, 1980
A:Title: Cloning of the rabbit uteroglobin structural gene.
A:Reference number: I46905; MUID:81021016; PMID:7417250
A:Accession: I46905
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 39-77 <CH2>
A:CROSS-references: GB:M25057; NID:g165802; PIDN:AAA31498.1; PID:g165803
R:Suske, G.; Menne, C.; Cato, A.; Wenz, M.; Beato, M.
Prog. Clin. Biol. Res. 85, 139-146, 1982
A:Title: Structure and regulated expression of the uteroglobin gene.
A:Reference number: I46907; MUID:82275176; PMID:6287481

A:Accession: I46907
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-45, 'V', '47-91 <SU2>
A:CROSS-references: GB:M32012; NID:g165807; PIDN:AAA31500.1; PID:g165809
R:Atger, M.; Perricaudet, M.; Tiollais, P.; Milgrom, E.
Biochem. Biophys. Res. Commun. 93, 1082-1088, 1980
A:Title: Bacterial cloning of the rabbit uteroglobin structural gene.
A:Reference number: I46906; MUID:80241888; PMID:6156676
A:Accession: I46906
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 53-66, 'NT', '69-72 <AT2>
A:CROSS-references: GB:M25038; NID:g165804; PIDN:AAA31499.1; PID:g165805
C:Comment: Uteroglobin is secreted by the uterus upon induction by progesterone. It b
A:Genetics:
A:Introns: 19/1; 81/3
C:Complex: homodimer linked by two disulfide bonds
C:Superfamily: uteroglobin
F:1-21/Domain: signal sequence #status experimental <SIG>
F:22-91/Product: uteroglobin #status experimental <MAT>
F:24/Disulfide bonds: interchain (to 90) #status experimental
F:90/Disulfide bonds: interchain (to 24) #status experimental
Query Match 16.4%; Score 89; DB 1; Length 91;
Best Local Similarity 27.8%; Pred. No. 0.026;
Matches 27; Conservative 18; Mismatches 36; Indels 16; Gaps 3;
QY 1 MKGSRALLVALTLFC-----TCRMATGEDNDEFFMDFLQTLVLGTPPELYEGTGLKYN 54
DB 1 MKLAITLALVTLALLCSPASAGICPR-----FAHVIEILLLTGPSS-YETSLKEFE 50
QY 55 VNEDAKAAATELKSICIDGLQPMHKAELVLLVQVLGS 91
DB 51 PDDTMKDAQMQMKVLDLSPQTTRENTMKLTEKIVKS 87
RESULT 6
UGMS
N:Alternate names: CC10; Clara cell 10K protein precursor; Clara cell secretory prote
C:Species: Mus musculus (house mouse)
C:Date: 03-May-1994 #sequence_revision 21-Jan-1997 #text_change 22-Jun-1999
C:Accession: A53025; A56656; I51925; S24783
R:Stripp, B.R.; Huffman, J.A.; Bohinski, R.J.
Genomics 20, 27-35, 1994
A:Title: Structure and regulation of the murine Clara cell secretory protein gene.
A:Reference number: A53025; MUID:94292183; PMID:8020953
A:Accession: A53025
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-96 <STR>
A:CROSS-references: GB:L24372; NID:g461147; PIDN:AAA65446.1; PID:g785054
R:Singh, G.; Katyal, S.L.; Brown, W.E.; Kennedy, A.L.
Exp. Lung Res. 19, 67-75, 1993
A:Title: Mouse Clara cell 10-kDa (CC10) protein: cDNA nucleotide sequence and molecu
A:Reference number: A56656; MUID:93178380; PMID:8440203
A:Accession: A56656
A:Molecule type: mRNA; protein
A:Residues: 1-96 <SIN>
A:CROSS-references: EMBL:X67702; NID:g49690; PIDN:CAA47936.1; PID:g49691
A:Experimental source: lung
A:Note: sequence extracted from NCBI backbone (NCBIP:126148)
R:Margraf, L.R.; Finegold, M.J.; Stanley, L.A.; Major, A.; Nawkins, H.K.; DeMayo, F.J.
Am. J. Respir. Cell Mol. Biol. 9, 231-238, 1993
A:Title: Cloning and tissue-specific expression of the cDNA for the mouse Clara cell
A:Reference number: I51925; MUID:94000840; PMID:8398159
A:Accession: I51925
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-96 <RES>

GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: May 14, 2003, 10:50:34 ; Search time 17.5 seconds
(without alignments)
593.771 Million cell updates/sec

Title: US-09-768-826-47

Perfect score: 542
Sequence: 1 MKGSRALLVLTFCICRM.....VQVLGSDGAGIDYKDDDDK 105

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR_73.*
2: PIR_73.*
3: PIR_73.*
4: PIR_73.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	349.5	64.5	94	2 S17449	probable ligand-bi
2	96.5	17.8	96	2 A36581	polychlorinated bi
3	92	17.0	91	2 JS0036	Clara cell 10K pro
4	91	16.8	95	2 S68231	FHC22 protein prec
5	89	16.4	91	1 UGRB	uteroglobin precu
6	81.5	15.0	96	1 UGMS	uteroglobin precu
7	80	14.8	91	1 UGRBL	uteroglobin precu
8	78.5	14.5	113	2 JC2026	cell specific 10K
9	76.5	14.1	504	2 S05197	signal recognition
10	76.5	14.1	504	2 S05198	signal recognition
11	76.5	14.1	504	2 S54143	SRP 54 protein - h
12	73	13.5	609	2 T38656	probable RNA-bind
13	70.5	13.0	423	2 S41122	mannose-6-phosphat
14	69.5	12.8	2458	2 T17420	probable polyketid
15	69	12.7	540	2 G86790	fibronectin-bindin
16	68.5	12.6	2100	2 T38128	t7123.15 protein -
17	68	12.5	92	2 A56413	major allergen Fel
18	68	12.5	270	2 S30947	hypothetical prote
19	67.5	12.5	299	2 T16337	hypothetical prote
20	67.5	12.5	322	2 C83075	octaprenyl-diphosp
21	67.5	12.5	1953	2 S63244	BNII protein - yea
22	67	12.4	511	2 T02269	hypothetical prote
23	66.5	12.3	358	2 AD3580	iron(III)-binding
24	66	12.2	192	2 S70285	outer surface prot
25	65.5	12.1	192	2 JC1136	major allergen Cha
26	65.5	12.1	122	2 A43644	sarcocystatin A pr
27	65.5	12.1	362	2 A71243	probable maltose/m
28	65.5	12.1	1321	2 T10929	3C3.20c protein -
29	65.5	12.1	1687	2 T30244	phosphodiesterase

30	65.5	12.1	1706	2 T30175	exoribonuclease, v
31	65.5	12.1	1719	2 T30174	exoribonuclease, v
32	65	12.0	209	2 S73690	MG331 homolog P01
33	65	12.0	255	2 B64175	repressor modE hom
34	65	12.0	312	2 G71146	hypothetical prote
35	65	12.0	842	2 E96641	hypothetical prote
36	65	12.0	2233	1 ZLN2P3	genome polyprotein
37	64.5	11.9	339	2 E90436	coA-ligase / coenz
38	64.5	11.9	403	2 B89808	hypothetical prote
39	64.5	11.9	454	1 XNRTV	tyrosine transamin
40	64.5	11.9	518	2 H85440	cytochrome P450-11
41	64.5	11.9	882	1 WMBEUS	gene UL5 protein -
42	64	11.8	190	2 T20725	hypothetical prote
43	64	11.8	342	1 C69395	H+-transporting AT
44	64	11.8	446	2 G81326	probable DNA repai
45	64	11.8	627	2 H96951	fusion, PTS system

ALIGNMENTS

RESULT 1

S17449

probable ligand-binding protein RYD5 - rat

C:Species: Rattus norvegicus (Norway rat)

C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Nov-1999

C:Accession: S17449

R:Dear, T.N.; Boehm, T.; Keverne, E.B.; Rabbitts, T.H.

EMBO J. 10, 2813-2819, 1991

A:Title: Novel genes for potential ligand-binding proteins in subregions of the olfac

A:Reference number: S17447; MUID:92007724; PMID:1915264

A:Accession: S17449

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-94 <DEA>

A:Cross-references: EMBL:X60661; NID:g57735; PIDN:CAA43068.1; PID:g57736

Query Match

Best Local Similarity

Matches 70; Conservative 11; Mismatches 11; Indels 1; Gaps 1;

QY

1 MKGSRALLVLTFCICRMATGDNDEFMDLQTLVLTGTPPELYEGLGKYNVDNAK 60

1 MKGSSA-LLVALTVLCICGLTFAEDDNEFFMEFLQTLVLTGTPPELYEGLGKYNVDNAK 59

QY

61 AAMTELKSCIDGLQPMHKAELVLLVQLVLSQD 93

60 AALTELKSCIDELQPVHKEQLVLLVQLVDAQE 92

RESULT 2

A36581

polychlorinated biphenyl-binding protein precursor - rat

N:Alternate names: Clara cell 10K secretory protein

C:Species: Rattus norvegicus (Norway rat)

C>Date: 08-Mar-1991 #sequence_revision 08-Mar-1991 #text_change 20-Aug-1999

C:Accession: A36581; S10185; S21676

R:Nordlund-Moeller, L.; Andersson, O.; Ahlgren, R.; Schillling, J.; Gillner, M.; Gusta

J. Biol. Chem. 265, 12690-12693, 1990

A:Title: Cloning, structure, and expression of a rat binding protein for polychlorina

A:Reference number: A36581; MUID:90324266; PMID:2115524

A:Accession: A36581

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-96 <NOR>

A:Cross-references: GB:J05536; NID:g206039; PIDN:AAA41817.1; PID:g206040

R:Hagen, G.; Wolf, M.; Katyal, S.L.; Singh, G.; Beato, M.; Suske, G.

Nucleic Acids Res. 18, 2939-2946, 1990

A:Title: Tissue-specific expression, hormonal regulation and 5'-flanking gene region

A:Reference number: S10185; MUID:90272398; PMID:2349092

A:Accession: S10185

A:Status: translation not shown

A:Molecule type: DNA

> O <
O| | O Intelligence
> O <

FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file 768826-47_x.res made by spaula on Wed 14 May 10:07:16-PDT.

Query sequence being compared: US-09-768-826-47 (1-105)
Number of sequences searched: 12
Number of scores above cutoff: 12

Results of the initial comparison of US-09-768-826-47 (1-105) with:
File : r55778.seq
File : x60661.seq

100 -

N -

U -

M -

B -

E -

R -

O -

F -

S -

E -

Q -

U -

E -

N -

C -

E -

S -

SCORE 0

STDEV 0

1 14 1 21 28 36 43 50 57 64

1 1 1 1 1 1 1 1 1 1

1 1 1 1 1 1 1 1 1 1

1 1 1 1 1 1 1 1 1 1

1 1 1 1 1 1 1 1 1 1

PARAMETERS

Similarity matrix Unitary K-tuple 2
Translation Frame 6
Mismatch penalty 1 Joining penalty 20
Gap penalty 1.00 Window size 105
Gap size penalty 0.05
Cutoff score 0
Randomization group 0

SEARCH STATISTICS

Scores: Mean Median Standard Deviation
9 5 17.19

Times: CPU 00:00:00.00
Total Elapsed 00:00:00.00

Number of residues: 1690
Number of sequences searched: 12
Number of scores above cutoff: 12

The scores below are sorted by initial score.
Significance is calculated based on initial score.
A 100% identical sequence to the query sequence was not found.

The list of best scores is:

Sequence Name	Description	Length	Opt. Score	Init. Opt.
1. x60661	*** 3 standard deviations above mean *** TOIG of: x60661 check: 2527	145	64	70
2. x60661	*** 0 standard deviation from mean *** TOIG of: x60661 check: 2527	144	7	21
3. x55778	TOIG of: x55778 check: 2244	137	5	15
4. x60661	TOIG of: x60661 check: 2527	143	5	22
5. x60661	TOIG of: x60661 check: 2527	143	5	18
6. x60661	TOIG of: x60661 check: 2527	144	5	19
7. x55778	TOIG of: x55778 check: 2244	137	4	12
8. x55778	TOIG of: x55778 check: 2244	138	4	13
9. x55778	TOIG of: x55778 check: 2244	138	4	16
10. x55778	TOIG of: x55778 check: 2244	138	4	10
11. x55778	TOIG of: x55778 check: 2244	139	4	14
12. x60661	TOIG of: x60661 check: 2527	144	3	16

1. US-09-768-826-47 (1-105)
TOIG of: x60661 check: 2527 from: 1 to: 435

Initial Score = 64
Residue Identity = 67%
Gaps = 1
Translation Frame = 1
Optimized Score = 70
Significance = 3.20
Matches = 33
Mismatches = 0
Conservative Substitutions = 0

X 10 20 30 40 50 60
MKGRALLVALLVLCICRMATGEDNDEFFMDLQTLVGPPELYEGTIGKYNNEDAKAAMTELKS
VVTVMKGSSA-LLVALLVLCICGLTRAEDEFFMEFLQTLVGPPELYEGTIGKYNNEDAKAAMTELKS
X 10 20 30 40 50 60 70

70 80 90 100 X
CIDGLQPMHKAELVLLVQVLSGQDAGTDYRDDDDK
CIDEQPVHKEQLVLLVQVLSGQDAGTDYRDDDDK
80 90 100 110 120 130 140
SP

2. US-09-768-826-47 (1-105)
TOIG of: x60661 check: 2527 from: 1 to: 435

Initial Score = 7
Residue Identity = 23%
Gaps = 16
Translation Frame = 4
Optimized Score = 21
Significance = -0.12
Matches = 26
Mismatches = 70
Conservative Substitutions = 0

X 10 20 30
MKGRALLVALLVLCICRMATGEDNDEFFMDLQTL
WTALDFIDLVGRXIYWRSTGLSTSMATCTAGPIARRGQAMFWGLCVLLSIXHLHQDLQDLLLHRLQFI
40 50 60 70 80 90 100 110 120 130 140
LVGTPEELYEGTIGKYNNEDAKAAMTEL--KSCIDGLQPMHKAELVLLVQVLSGQDAGTDYRDDDDK
NAG--LELCQRCGLGHVIDIVLAQGPFIELFWGPHQECLOEFH-----EKLIVILCSSQ---PTDAEHGXSHOK
SAAPFHDSH
140

3. US-09-768-826-47 (1-105)
TOIG of: r55778 check: 2244 from: 1 to: 417

Initial Score = 5
Optimized Score = 15
Significance = -0.23

```
Residue Identity = 21% Matches = 24 Mismatches = 56
Gaps = 32 Conservative Substitutions = 0
Translation Frame=
6
10 X 20 30 40 50 60
MKGSRALLVLTLCICRMATGDNDEFFMDFLQTLVGTPEELYEGTLGKYNVNEDAKAAMT---ELKS-
TRF---SVETG---QIPYPXNPKGQGWAEIKWEPNRHK-----EGRLQGTGSPKLSL
X 10 20 30 40
70 80 90 100 110
----CIDGLQPMHKAELVKLL-----VQVLGS-----QDAGTDYKDDDK
LOIPARPGRAPGHW---VSHLPGNRCLPLPSLEASSPQHRGCVPGSXAXASCSHDPFPHDAPSSVV
50 60 70 80 90 100 110
NAAPCPGDRRTMLNVKK
120 130
4. US-09-768-826-47 (1-105)
x60661 TOIG Of: x60661 check: 2527 from: 1 to: 435
Initial Score = 5 Optimized Score = 22 Significance = -0.23
Residue Identity = 23% Matches = 26 Mismatches = 78
Gaps = 8 Conservative Substitutions = 0
Translation Frame=
6
X 10 20 30 40 50 60
MKGSRALLVLTLCICRMATGDNDEFFMDFLQTLVGTPEELYEGTLGKYNVNEDAKA--
DCIRLYAFNSRNLVKKHWSXHIHGVYGSVCSORSSHVLGLL-MCPLEHALAPAXPVAPYAAVH
10 20 30 40 50 60 70
70 80 90 100 110
--WTELKSCIDGLQPMHKAELVKLLVQVLGSQDG--AGTDYKDDDK
QCRTXALSALPWPCHXCTCPGALHRLGSPGCVFAGIPKXTHCHPLLXSAHRCRARLEPPEERCSSXS
80 90 100 110 120 130 140
5. US-09-768-826-47 (1-105)
x60661 TOIG Of: x60661 check: 2527 from: 1 to: 435
Initial Score = 5 Optimized Score = 18 Significance = -0.23
Residue Identity = 19% Matches = 22 Mismatches = 76
Gaps = 15 Conservative Substitutions = 0
Translation Frame=
5
X 10 20 30 40 50 60
MKGSRALLVLTLCICRMATGDNDEFFMDFLQTLVGTPEELYEGTLGKYNVNEDAKAAMT-ELKSC--
GLHXTLLIXQFEGEFTGEALVLAHPWPRVRLVLLAE-VKPCGAAVYSSXASSTCTSSITSCSL
X 10 20 30 40 50 60
70 80 90 100 110
-----IDGLQPMHKAELVKLLVQVL-----GSQDAGTDYKDDDK
CTGSSSMODLSSVSAALAMSLTLYLPRGFSXSSSGVPTRSVCRNKMNSLSSALVSPQMOSTVTRARL
70 80 90 100 110 120 130
LPFWTV
140
6. US-09-768-826-47 (1-105)
x60661 TOIG Of: x60661 check: 2527 from: 1 to: 435
Initial Score = 5 Optimized Score = 19 Significance = -0.23
Residue Identity = 21% Matches = 28 Mismatches = 62
Gaps = 39 Conservative Substitutions = 0
Translation Frame=
3
10 X 20 30 40 50 60
MKGSRALLVLTLCICRMATGDNDEFFMDFLQTLVGTPEELYEGTLGK-YVNVNDAKA-A-----
FFLTFTNIVLLSPG-QNAAP-----TTEENGASCGGKSGCWEHREAXAQDPGTPQR
```

```
X 10 20 30 40 50 60 70
MKGSR-RALLVA-----LTLFCICRMAT-GED-----NDEFFMDFLQTL
CDCHEREORSSGSRALHLWADXSXGXVFGHPANTGDPRRALXRAPGVQCOXHGCGSADRQVLH
10 20 30 40 50 60 70
40 50 60 70 80 90 100 110
VGTPEELYEGTLGKYNVNEDAKAAMTELKSCIDGLQPMHKAELVKLLVQVLGSQDAGTDYKDDDK
XXT-----AAGAXGATGQAAGASA-----RCSRGHISSPKTLW-DLCEQ-----XDQPYTPWMCXDCFFTS
80 90 100 110 120 130
KFTLELLNQXSLMOS
130 140
```

7. US-09-768-826-47 (1-105)
r55778 TOIG Of: r55778 check: 2244 from: 1 to: 417

Initial Score = 4 Optimized Score = 12 Significance = -0.29
Residue Identity = 15% Matches = 18 Mismatches = 81
Gaps = 21 Conservative Substitutions = 0
Translation Frame=

```
X 10 20 30 40 50
MKGSRALLVLTLCICRMATGDNDEFFMDFLQTLVGTPEELYEGTLGKYN
NPFCRGNPLPLSLKXPRAGLXNQMGTLQTXGRPKAARNGVVVXTAXSPSPNPGPTWKGGAL-GGPPPPWQ
10 20 30 40 50 60 70
60 70 80 90 100
VNEDAKAAMTELK-----CIDGL---QPM-HKAELVKL-----LVQVLGSQDAGTDYKDDDK
VSVSPALARGLFSPAPLWCAGTSLGLPMFPAPXSLPATRCVSFFRCRVLXSWQENNVGERQK
80 90 100 110 120 130 140
```

8. US-09-768-826-47 (1-105)
r55778 TOIG Of: r55778 check: 2244 from: 1 to: 417

Initial Score = 4 Optimized Score = 13 Significance = -0.29
Residue Identity = 27% Matches = 19 Mismatches = 28
Gaps = 22 Conservative Substitutions = 0
Translation Frame=

```
X 10 20
MKGSRALLVLTLCICRMAT
LGSGSRHTTAVLGRGRLERGQGTAPRIAREVAHRVPGRPSRSGRGLKFGFKRSRPSLQPL----AFLMSG
50 60 70 80 90 100
30 40 50 60 70 80 90
GENDEFFMDFLQTLVGTPEELYEGTLGKYNVNEDAKAAMTELKSCIDGLQPMHKAELVKLLVQVLGSQDG
G-----FPFDFSPT-----LPFRVLG---IRED---LARLDKSG
110 120 130 140
```

AGTDYKDDDK

9. US-09-768-826-47 (1-105)
r55778 TOIG Of: r55778 check: 2244 from: 1 to: 417

Initial Score = 4 Optimized Score = 15 Significance = -0.29
Residue Identity = 21% Matches = 23 Mismatches = 60
Gaps = 25 Conservative Substitutions = 0
Translation Frame=

```
10 20 30 40 50 60
MKGSRALLVLTLCICRMATGDNDEFFMDFLQTLVGTPEELYEGTLGK-YVNVNDAKA-A-----
FFLTFTNIVLLSPG-QNAAP-----TTEENGASCGGKSGCWEHREAXAQDPGTPQR
```

10. US-09-768-826-47 (1-105)
r55778 TOIG of: r55778 check: 2244 from: 1 to: 417
Initial Score = 4 Optimized Score = 10 Significance = -0.29
Residue Identity = 19% Matches = 12 Mismatches = 47
Gaps = 3 Conservative Substitutions = 0
Translation Frame= 4
FMGXGKIWPVXTENRV
130

11. US-09-768-826-47 (1-105)
r55778 TOIG of: r55778 check: 2244 from: 1 to: 417
Initial Score = 4 Optimized Score = 13 Significance = -0.29
Residue Identity = 16% Matches = 17 Mismatches = 68
Gaps = 17 Conservative Substitutions = 0
Translation Frame= 1
MKGSRALLVATLFCICRMAT
130

12. US-09-768-826-47 (1-105)
x60661 TOIG of: x60661 check: 2527 from: 1 to: 435
Initial Score = 3 Optimized Score = 16 Significance = -0.35
Residue Identity = 16% Matches = 24 Mismatches = 77
Gaps = 41 Conservative Substitutions = 0
Translation Frame= 2
MKGSRALLVATLFCICRMATGEDNDEFMDFLQ--TLVGTPEELYEGTLGKYNVEDAKAAMTELKSC
130

60 KAAM-----TELKSCIDGLOPM-----HKAELVKLLVOVLGSDGAGTDYKDDD
100
PALMNCSCRCIRSNWSSCWCKCXXMLKRTHKOPQNMXPPLRAIGPAVHVAMDV--LRPVLHGXIHPTVKSIIK
80 90 100 110 120 130 140
X
DK
SNAV
X

13. US-09-768-826-47 (1-105)
r55778 TOIG of: r55778 check: 2244 from: 1 to: 417
Initial Score = 4 Optimized Score = 10 Significance = -0.29
Residue Identity = 19% Matches = 12 Mismatches = 47
Gaps = 3 Conservative Substitutions = 0
Translation Frame= 4
FMGXGKIWPVXTENRV
130

14. US-09-768-826-47 (1-105)
r55778 TOIG of: r55778 check: 2244 from: 1 to: 417
Initial Score = 4 Optimized Score = 13 Significance = -0.29
Residue Identity = 16% Matches = 17 Mismatches = 68
Gaps = 17 Conservative Substitutions = 0
Translation Frame= 1
MKGSRALLVATLFCICRMATGEDNDEFMDFLQ--TLVGTPEELYEGTLGKYNVEDAKAAMTELKSC
130

15. US-09-768-826-47 (1-105)
x60661 TOIG of: x60661 check: 2527 from: 1 to: 435
Initial Score = 3 Optimized Score = 16 Significance = -0.35
Residue Identity = 16% Matches = 24 Mismatches = 77
Gaps = 41 Conservative Substitutions = 0
Translation Frame= 2
MKGSRALLVATLFCICRMATGEDNDEFMDFLQ--TLVGTPEELYEGTLGKYNVEDAKAAMTELKSC
130

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